

Figure 1

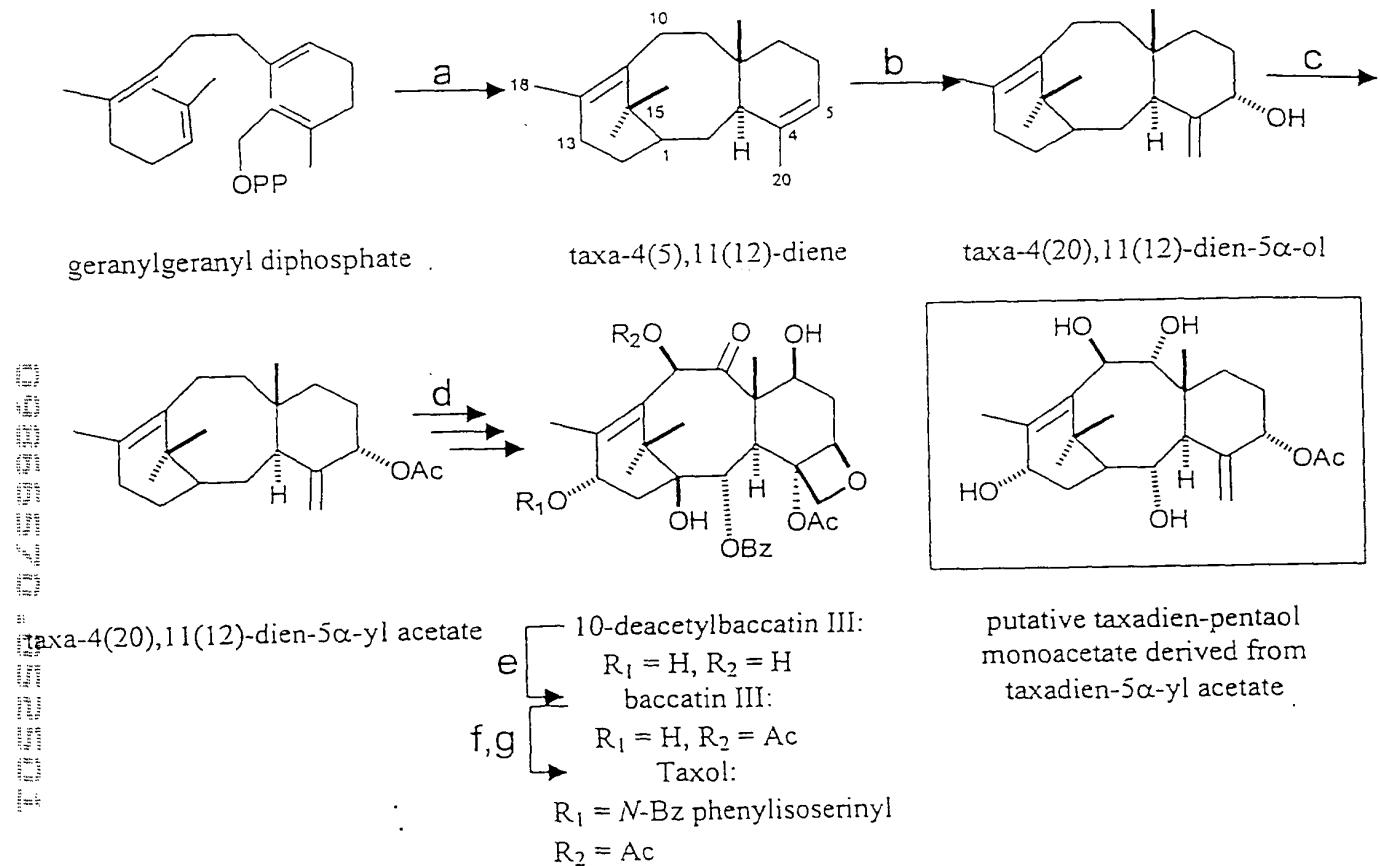


Figure 2

Tryptic Peptide Fragment	Peptide Sequence
SEQ ID NO: 29	TTLQLSSIDNLPGVR
SEQ ID NO: 30	ILVYYPPFAGR
SEQ ID NO: 31	FTCGGFVVGVSF
SEQ ID NO: 32	KGLAEIARGEVK
SEQ ID NO: 33	NLPNDTNPSSGYYGN

Figure 3

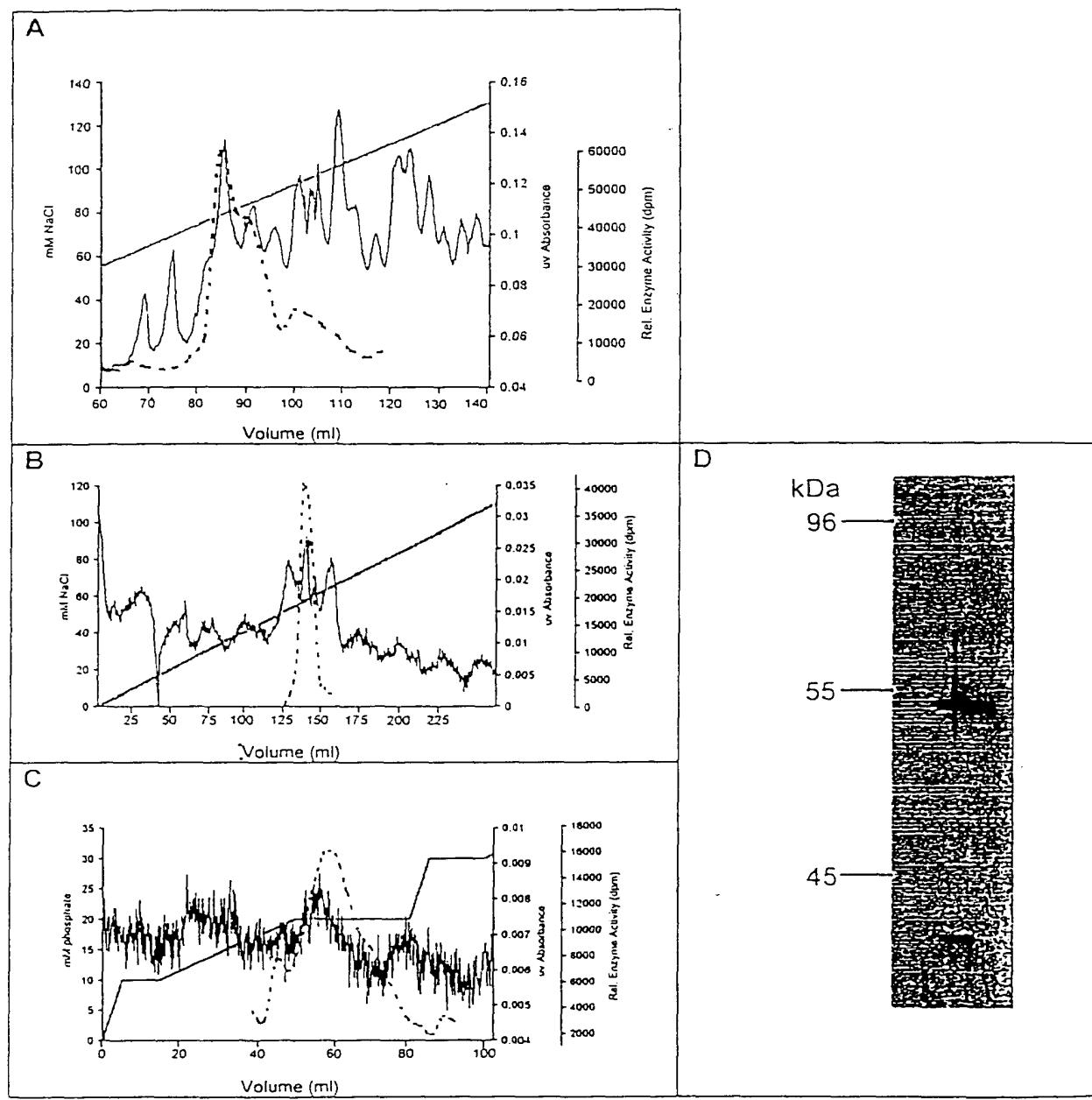


Figure 4

FROM PEPTIDE FRAGMENT SEQUENCE 2

NH₂- I L V Y Y P P -COOH
5' ATI CTI GTI TAT TAT CCI CC 3'
T C C C C
A A

AT-FOR1

(SEQ ID NO: 34)

NH₂- Y Y P P F A G -COOH
5' TAT TAT CCI CCI TTT GCI GG 3'
C C C C C C
A A A

AT-FOR2

(SEQ ID NO: 35)

FROM SEQUENCE HOMOLOGY CONSIDERATIONS

NH₂- F Y P F A G R -COOH
5' TTC TAT CCI TTC GCI GGI AG 3'
T C T C C
A A

AT-FOR3

(SEQ ID NO: 36)

NH₂- Y Y P L A G R -COOH
5' TAC TAT CCI TTI GCI GGI AG 3'
T C C C C C
A A

AT-FOR4

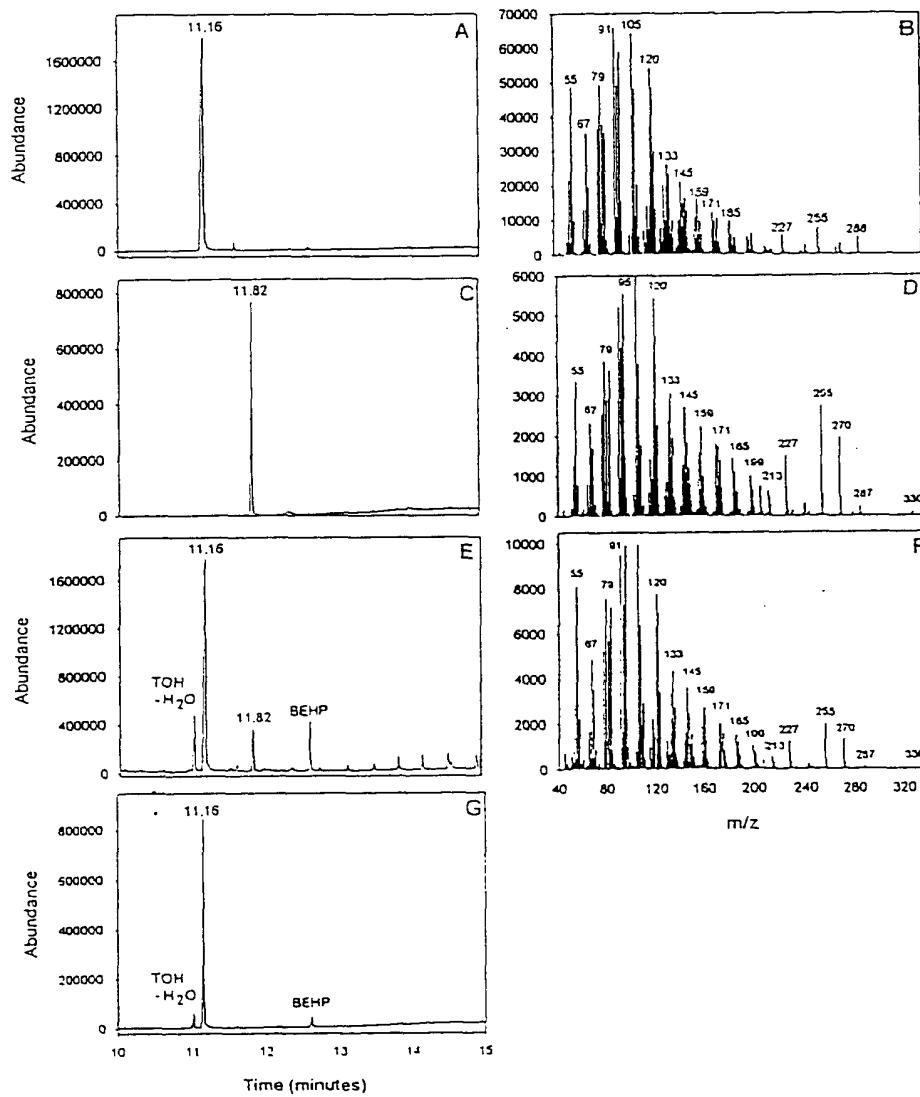
(SEQ ID NO: 37)

NH₂- D F G W G K P -COOH
3' CTA AAA CCI ACC CCI TTT GG 5'
G G C C C
A A

AT-REV1

(SEQ ID NO: 38)

Figure 5



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TAXI KTTDOL851D MNGVGRSIF NALIYHNSP SPTMISADP. AKTI RELEKITYV YPSEAGRD R ETENG 90
TAXI KURL18P1D HKT. RGLT HILSYVHNSO RVS. VSADP. AKTI RELEKITYV YPSEAGRD R NTENG 84
ab61523 KRTNBLD LISSPMYTG ALFVLAADPQH LUGFSTET. SLKE KKSLEKTRPI YPSEAGRD R 0
ab65293 DLTLSVBDL HILSCMHIOKG CLFCPH. LPLPAI. ISHE KHSLSITR H PPLAORES. TSSC 86
ab61523 HSLYLVHNSP DLRGARVTP SYVYPSHTH RESVY. LKNE QDASDEVY YPSEAGRD R EYENG 100
ab617079 H LPLBMLD HILPRLVH CFCYKKP. LHTDNTVA. YETKU LAETVS YPSEAGRD R TMPTC 208
anc08021 LOKMLBLD QTOFPYVGL IFLHY. E TLSDNGD. LSKL ESGLETLT YPSEAGRD R 79
anc27152 RKSMLBLD QLHN. FDV QTVNFFRPNK EFFRHM. SKED HKLVKLDA YPSEAGRD R DRSG 97
anc9331 L.SRYHLYND QHIVQTCVSV GFFYEHPGI EISTIRE. QD QHSLEKTLVS YPSEAGRD R 87
ad61205 . GNEPVAEHD QV. GTITHI OTLYFOKPS LSFQGHV. VIE KTSLSRVH YPSEAGRD R LP.RG 82
cn20531 . ETLSMLBLD HOPFHENVYA TIVYFKNGK HLD. DP. VSLR KNLSELVH YPSEAGRD R SESNC 92
can6656 NETKFLDID DQEGIN. F QIPVIQFYK DSSIGKDP. VKVJ KKAIAETLVF YPSEAGRD R EGNC 92
cn20412 YEFKOLADP DOOSIR. L QLPVHIVPH HPSLFRGDP. VKVJ KELIGKAVF YPSEAGRD R EGPR 05
cnb6327 . KSTLWLMID HILRTPYSH GAVLIYKQD HN. EDHINPS SSIMYFDAHII YPSEAGRD R IN GD 90
cnb1010 . QTLTOLGTYD HILPPVYTA FLFYTKNL. ISOCHT. SHKU KTSUBETLK YPSEAGRD R 05
cnb1039 R LOSIHD LYCPGIVYST IFFY. O LITESSEV. SENH KLSJETSR YPSEAGRD R 79
cnb0761 HDKKLTLS HLDRCPLH YSVFFYKWT TROFDSV. PSHD KLGEEETLS YPSEAGRD R DGGC 09

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TAX1 . C S .. S F E V A S A H T W I L A R T A A F Q I P E S E Y	V K I L F G H O M R U S F N P . P L U P S G V I O N S I G T A C A V D H V O D	314
TAX2 . F S .. A F F E V V V A H L I H A R T K S F R I P P H E Y	V K I L F G H O M R U S F N P . P L U P S G V I O N A I G H A C A M D H V O D	308
ab61522 R V E V I S V F I M R S F H A S T H D D K T C K Y T V K I L F G H O M R U S F N P . P L U P S G V I O N H I R F S V T V T H M I H	N I R F S V T V T H M I H	197
ab61523 R V E V I T A L F H R C V T K V S R S S L T P R T S V V K I L F G H O M R U S F N P . P L U P S G V I O N C E N T R I C N . H I S L M I	N I R F S V T V T H M I H	104
ab61523 A V E I S S F O S I C A L I H R A I T R A R K L P S S K T T V K I L F G H O M R U S F N P . P L U P S G V I O N K L U P E V I O N A I	N I R F S V T V T H M I H	340
ab61523 V C S .. T F D A M A H I M R S W V K A L D V R P D Y H V K I L F G H O M R U S F N P . P L U P S G V I O N V U C L A C A M S S V E S	N I R F S V T V T H M I H	339
act1079 K E S F S A F L N K I V A E H A K O P U R I K T S K V K I L F G H O M R U S F N P . P L U P S G V I O N K E N T T E C N V A L S V P F G Q R I D D I	N I R F S V T V T H M I H	427
act10062 R V D V I V T A F L S K S L E M D C A K K E Q T S R P S L V K I L F G H O M R U S F N P . P L U P S G V I O N K E N T T E C N V A L S V P F G Q R I D D I	N I R F S V T V T H M I H	101
act27152 H V R V T G F H V V T A I V H R C K A L S V A A E G E T V K I L F G H O M R U S F N P . P L U P S G V I O N N A V I T A Y A K E K C X A	N I R F S V T V T H M I H	337
act69311 R V E V I T A F L S R C A T V A G K S A A K H H C G Q S U P F F V V Q A T H R P I L E V K I L F G H O M R U S F N P . P L U P S G V I O N N U V I Y F S R T I K E N D	N I R F S V T V T H M I H	309
act12023 A K G F T R Y C T V T G H V H V C A C K A R G H S P E Q T V K I L F G H O M R U S F N P . P L U P S G V I O N E P P L E R G T C T I O N A L T O D V A A S T S G E	N I R F S V T V T H M I H	323
can20531 R E S F T T Y E V V S Y Y I H K I N S R A L K L H P D G T V K I L F G H O M R U S F N P . P L U P S G V I O N N A Y I D V Y V E L T V R E	N I R F S V T V T H M I H	327
can64636 . C S .. T F E L L T A V I H R C R T H S K P D P E R V K I L F G H O M R U S F N P . P L U P S G V I O N N A F F R V A U T T A A K	N I R F S V T V T H M I H	322
can94412 . C P .. S F E V I T A V I H R C R T H A L Q F K P E E R V K I L F G H O M R U S F N P . P L U P S G V I O N N A V V V R A V T T A A K	N I R F S V T V T H M I H	314
can06427 I S T Y E V V A L H V H R E V G V S K A R G I S D H E E I V K I L F G H O M R U S F N P . P L U P S G V I O N N A V V V R A V T T A A K	N I R F S V T V T H M I H	324
cab10318 R V E S V T A I H R C F V K I L F G H O M R U S F N P . P L U P S G V I O N Q A N T A R S K I P S	N I R F S V T V T H M I H	300
cab10319 R V E A I H S I H R C A R U S S R S H U L I P R O A V V K I L F G H O M R U S F N P . P L U P S G V I O N Q A N T A R S K I P S	N I R F S V T V T H M I H	301
cab40761 . F H C S S F F F T A H L H K A T R A A L G I R R O A V K I L F G H O M R U S F N P . P L U P S G V I O N N A V V V A S V A S T A R E	N I R F S V T V T H M I H	341



Figure 6
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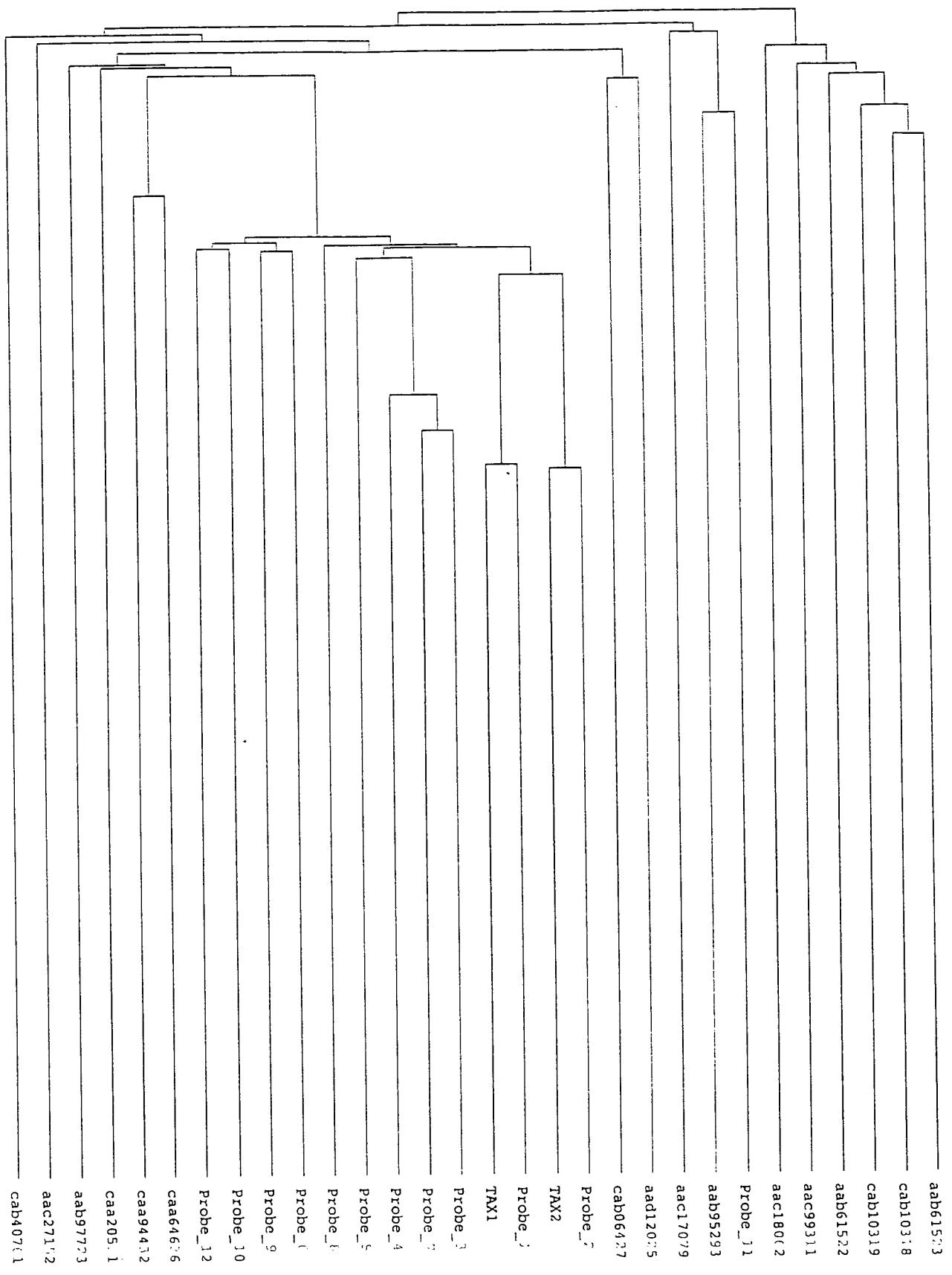


Figure 7

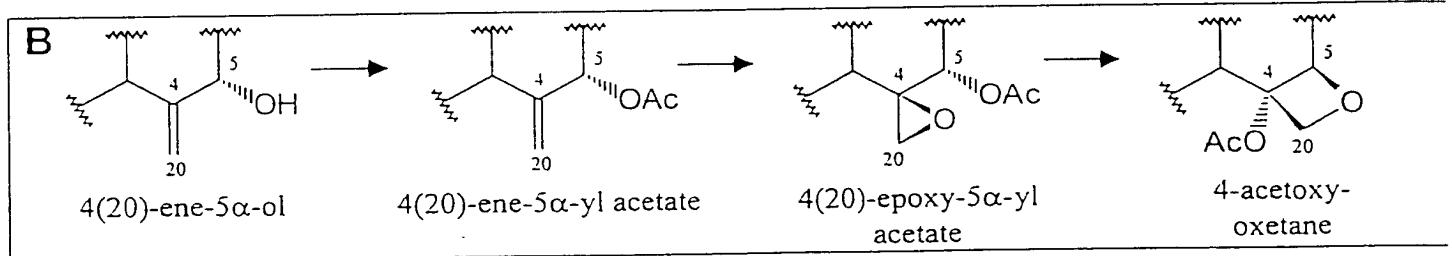
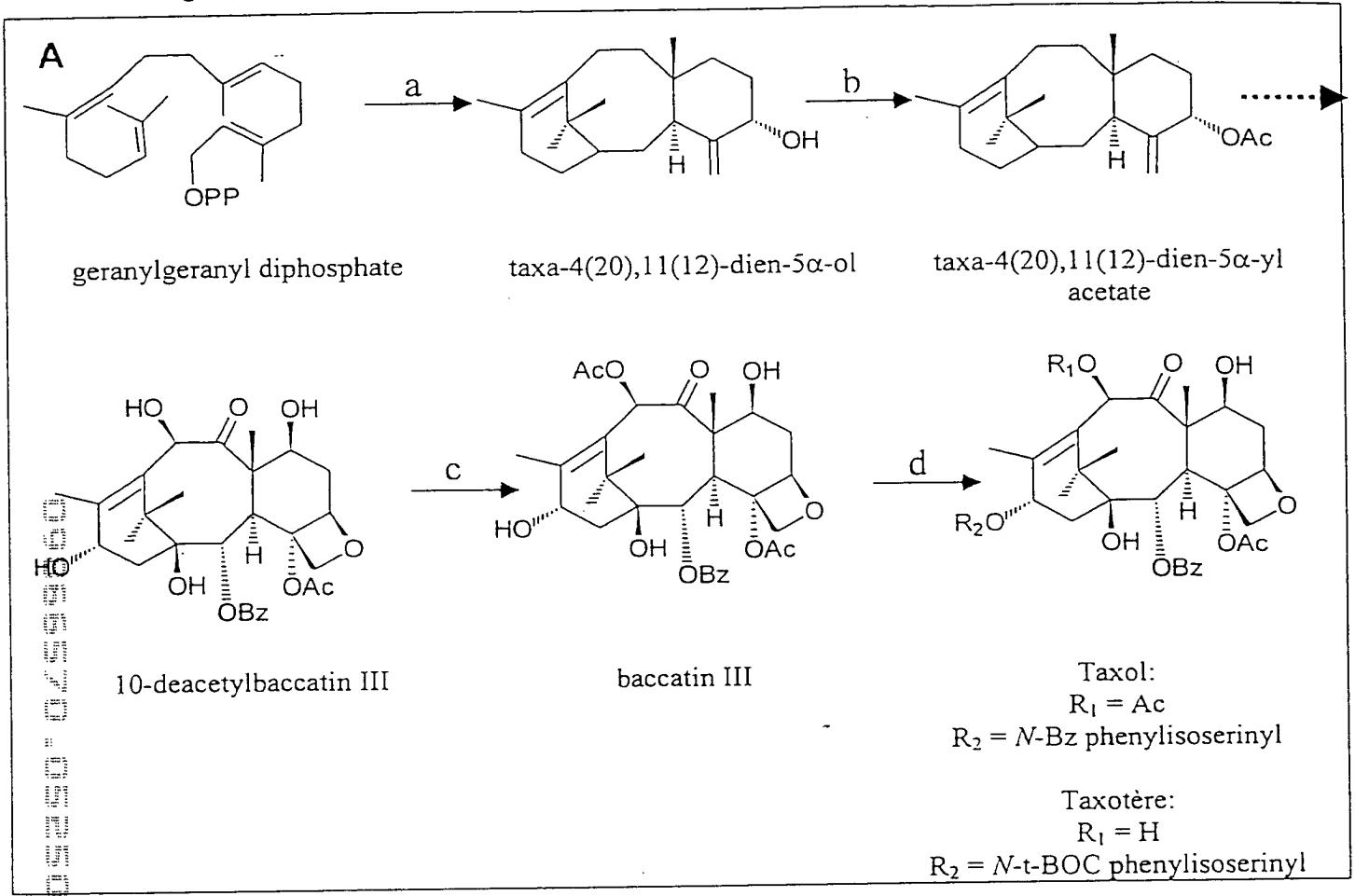
Figure 8

Figure 9

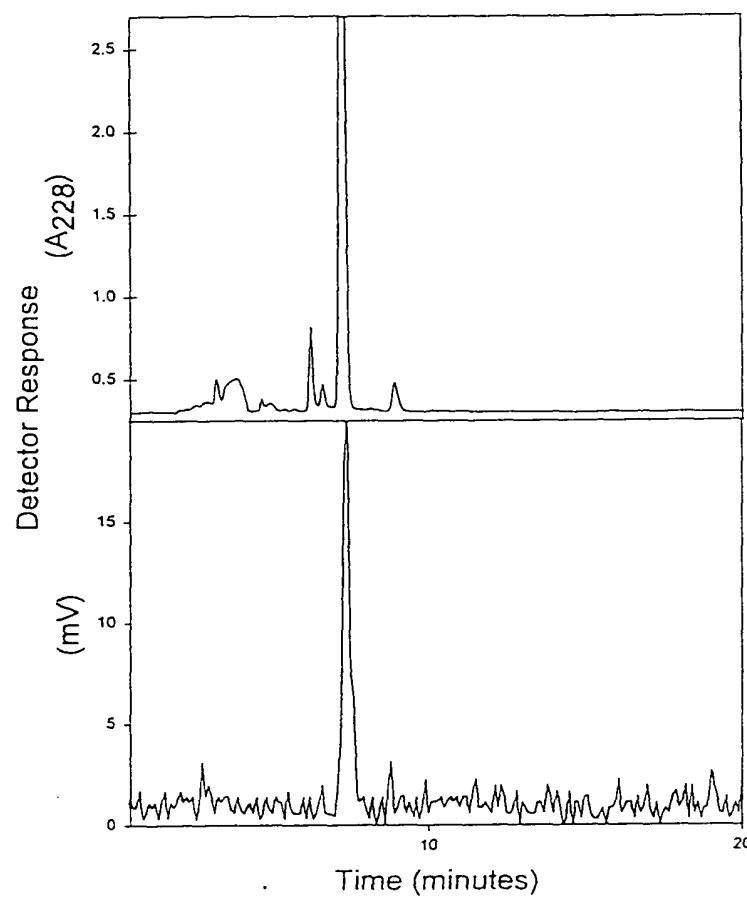


Figure 10

